

EXHIBIT 7

ATCC 31,195 ALPHA-AMYLASE AMINO ACID SEQUENCE

1 aapfngtmmq yfewylpddg tlwtkvanea nnlsslgita lwlppaykgt srsdvgygvy
61 dlydlgefng kgtvrtkygt kaqylqaiqa ahaagmqvya dvvfdhkqga dgtewvdave
121 vnpsdrnqei sgtyqiqawt kfdfpgrgnt yssfkwryw fdgvdwdesr klsriykfrg
181 igkawdwevd tengnydylm yadldmdhpe vvtelknwvk wyvnttnidg frldavkhik
241 fsffpdwlsy vrsqtgkplf tvgeywsydi nklhnyitkt ngtmlfdap lhnkfytask
301 sggafdmrtl mtntlmkdqp tlavtfvdnh dtepggalqs wdpwfkpla yafiltrqeg
361 ypcvfygdy gipqynipsi kskidpllia rrdyaygtqh dyldhsdiig wtregvtekp
421 gsglaalitd gpggskwnyv gkqhagkvfy dltgnrsdtv tinsdgwgef kvnggsvsvw
481 vprkttvst

EXHIBIT 8

GAP ALIGNMENT:
ATCC 31,195 Alpha-Amylase to Spezyme Ethyl (Old Matrix)

GAP of: NewC.pep check: 5818 from: 1 to: 489

WPDEF ATCC 31,195 ALPHA-AMYLASE AMINO ACID SEQUENCE
 None

to: SPEZE.pep check: 525 from: 1 to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
 None

Symbol comparison table: oldpep.cmp CompCheck: 2543
 Dayhoff table (Schwartz, R. M. and Dayhoff, M. O. [1979] in Atlas of Protein Sequence and Structure, Dayhoff, M. O. Ed, pp. 353-358, National Biomedical Research Foundation, Washington D.C.) rescaled by dividing each value by the sum of its row and column, and normalizing to a mean of 0 and standard deviation of 1.0. The value for FY (Phe-Tyr) = RW = 1.425. Perfect matches are set to 1.5 and no matches on any row are . . .

Gap Weight: 30 Average Match: 5.402
 Length Weight: 3 Average Mismatch: -3.964

Quality: 7224 Length: 489
 Ratio: 14.926 Gaps: 1
 Percent Similarity: 100.000 Percent Identity: 100.000

Match display thresholds for the alignment(s):
 | = IDENTITY
 : = 4
 . = 1

NewC.pep x SPEZE.pep June 11, 2005 12:05 ..

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      .
1 aapfngtmmqyfewylpddgtlwtkvaneannlssligitalwlppaykgt 50
  |||
1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50

      .
51 srsvdgygydlydlgefnqkgtvrtkygkqylqaiqaahaagmqvya 100
  |||
51 SRSDVGYGVDLYDLGEFNQKGTVRTKYGKQYLQAIQAAHAAGMQVYA 100

      .
101 dvvfdhkggadtewvdavevnpsdrnqeisgtyqiqawtkfdpgrgnt 150
  |||
101 DVVFDHKGGADEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150

      .
151 yssfkwrwyhfdgvdwdesrklsriykfrgigkawdwewdtengnydylm 200
  |||
151 YSSFKWRWYHFDGVDWDESRLSRIYKF..IGKAWDWEVDTENGNYDYL 198

      .
201 yadldmdhpevvvtelknwgkwyvnttnidgfrldavkhikfsffpdwlsy 250
  |||
199 YADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDVAVKHIFSFPPDWLSY 248
  
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GAP Alignment:
 ATCC 31,195 Alpha-Amylase to Spezyme Ethyl
 (Old Matrix)

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251 vrsqtgkplftvgeywsydinklhnyitktngtmslfdaplhmkfytask 300
    ||||||||||||||||||||||||||||||||||||||||||||||||
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298

301 sggafdmrtlmtntlmkdqptlavtfvdnhdtepggalqswvdpwfkpla 350
    ||||||||||||||||||||||||||||||||||||||||||||||||
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348

351 yafiltrqegypcvfygdyygipqynipslkskidplliarrdyaygtqh 400
    ||||||||||||||||||||||||||||||||||||||||||||||||
349 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398

401 dyldhsdiigwtregvtekpgsglaalitdgpggskwmyvgkqhagkvfy 450
    ||||||||||||||||||||||||||||||||||||||||||||||||
399 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448

451 dltgnrsdtvtinsdgwgefkvnggsvsvwvprkttvst 489
    ||||||||||||||||||||||||||||||||||||||||||||||||
449 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTT... 484

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EXHIBIT 9

GAP ALIGNMENT:
ATCC 31,195 Alpha-Amylase to Spezyme Ethyl (New Matrix)

GAP of: NewC.pep check: 5818 from: 1 to: 489

WPDEF ATCC 31,195 ALPHA-AMYLASE AMINO ACID SEQUENCE
 None

to: SPEZE.pep check: 525 from: 1 to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
 None

Symbol comparison table: blosum62.cmp CompCheck: 1102
 BLOSUM62 amino acid substitution matrix.
 Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
 substitution matrices from protein blocks. Proc. Natl. Acad.
 Sci. USA 89: 10915-10919.

Gap Weight: 8 Average Match: 2.778
 Length Weight: 2 Average Mismatch: -2.248

Quality: 2665 Length: 489
 Ratio: 5.506 Gaps: 1
 Percent Similarity: 100.000 Percent Identity: 100.000

Match display thresholds for the alignment(s):
 | = IDENTITY
 : = 2
 . = 1

NewC.pep x SPEZE.pep June 11, 2005 12:01 ..

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1 aapfngtmmqyfewylpddgtlwtkvaneannlsslgitalwlppaykgt 50
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50

51 srsdvgygyvdyldlgefngkgtvrtkygtkaqylqaiqaahaagmqvya 100
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
51 SRSDVGYGVDLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYA 100

101 dvvfdhkgggadgtewvdavevnpsdrngeisgtyqiqawtkfdfpgrgnt 150
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
101 DVVFDHKGGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150

151 yssfkwrrwyhfdgvdwdesrklsriykgfrgigkawdwedvtengnydylm 200
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
151 YSSFKWRWYHFDGVDWDESRKLSRIYKF..IGKAWDWEVDTENGNYDYL 198

201 yadldmdhpevvvtelknwgkwyvnttnidgfrldavkhikfsffpdwlsy 250
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
199 YADLDMDHPEVVTELKNWGKQWYVNTTNIDGFRLDVAVKHIFSFPPDWLSY 248

251 vrsqtgkplftvgeywsydinklhnyitktngtmslfdaplhnkfytask 300

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GAP Alignment:
 ATCC 31,195 Alpha-Amylase to Spezyme Ethyl
 (New Matrix)

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|||||
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298
      .
301 sggafdmrtlmtntlmkdqptlavtfvdnhdtepggalqswvdpwfkpla 350
      |||||
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348
      .
351 yafiltrqegypcvfygdyygipqynipslkskidplliarrrdyaygtqh 400
      |||||
349 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398
      .
401 dyldhsdiigwtregvtekpgsglaalitdgppggskwmyvgkqhagkvfy 450
      |||||
399 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448
      .
451 dltgnrsdtvtinsdgwgefkvnggsvsvwvprkttvst 489
      |||||
449 DLTGNRSDTVTINSDGWGEFKVNGGsvsvwvprktt... 484

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EXHIBIT 10

Alpha-Amylase Alignments

Spezyme	AAPFNGTMMQ	YFEWYLPDDG	TLWTKVANE	NNLSSLGITA	LWLPPAYKGT	50
SEQ ID NO:3	AAPFNGTMMQ	YFEWYLPDDG	TLWTKVANE	NNLSSLGITA	LWLPPAYKGT	50
Figure 1	AAPFNGTMMQ	YFEWYLPDDG	TLWTKVANE	NNLSSLGITA	LWLPPAYKGT	50
ATCC 31,195	AAPFNGTMMQ	YFEWYLPDDG	TLWTKVANE	NNLSSLGITA	LWLPPAYKGT	50

Spezyme	SRSDVGYG	DLVDLGEFN	Q	KGTVRTKYGT	KAQYLQAIQA	AHAAGMQVYA	100
SEQ ID NO:3	SRSDVGYG	DLVDLGEFN	Q	KGTVRTKYGT	KAQYLQAIQA	AHAAGMQVYA	100
Figure 1	SRSDVGYG	DLVDLGEFN	Q	KGTVRTKYGT	KAQYLQAIQA	AHAAGMQVYA	100
ATCC 31,195	SRSDVGYG	DLVDLGEFN	Q	KGTVRTKYGT	KAQYLQAIQA	AHAAGMQVYA	100

Spezyme	DVVFDHKGGA	DGTEWVDAVE	VNPSDRNQEI	SGTYQIQAWT	KFDFFPGRGNT	150
SEQ ID NO:3	DVVFDHKGGA	DGTEWVDAVE	VNPSDRNQEI	SGTYQIQAWT	KFDFFPGRGNT	150
Figure 1	DVVFDHKGGA	DGTEWVDAVE	VNPSDRNQEI	SGTYQIQAWT	KFDFFPGRGNT	150
ATCC 31,195	DVVFDHKGGA	DGTEWVDAVE	VNPSDRNQEI	SGTYQIQAWT	KFDFFPGRGNT	150

Spezyme	YSSFKWRWYH	FDGVDWDESR	KLSRIYKF**	IGKAWDWEVD	TENGNYDYLM	198
SEQ ID NO:3	YSSFKWRWYH	FDGVDWDESR	KLSRIYKFRG	IGKAWDWEVD	TENGNYDYLM	200
Figure 1	YSSFKWRWYH	FDGVDWDESR	KLSRIYKFRG	IGKAWDWEVD	TENGNYDYLM	200
ATCC 31,195	YSSFKWRWYH	FDGVDWDESR	KLSRIYKFRG	IGKAWDWEVD	TENGNYDYLM	200

Spezyme	YADLDMDHPE	VVTELKNWGK	WYVNTTNIDG	FRLDAVKHIK	FSFFPDWLSY	248
SEQ ID NO:3	YADLDMDHPE	VVTELKNWGK	WYVNTTNIDG	FRLDAVKHIK	FSFFPDWLSY	250
Figure 1	YADLDMDHPE	VVTELKNWGK	WYVNTTNIDG	FRLDAVKHIK	FSFFPDWLSY	250
ATCC 31,195	YADLDMDHPE	VVTELKNWGK	WYVNTTNIDG	FRLDAVKHIK	FSFFPDWLSY	250

Spezyme	VRSQTGKPLF	TVGEYWSYDI	NKLHNYITKT	NGTMSLFDAP	LHNKFYTASK	298
SEQ ID NO:3	VRSQTGKPLF	TVGEYWSYDI	NKLHNYITKT	NGTMSLFDAP	LHNKFYTASK	300
Figure 1	VRSQTGKPLF	TVGEYWSYDI	NKLHNYITKT	NGTMSLFDAP	LHNKFYTASK	300
ATCC 31,195	VRSQTGKPLF	TVGEYWSYDI	NKLHNYITKT	NGTMSLFDAP	LHNKFYTASK	300

Alpha-Amylase Alignments
Page 2 of 2

Spezyme	SGGAFDMRTL	MTNTLMKDQP	TLAVTFVDNH	DTEPGQALQS	WVDPWFKPLA	348
SEQ ID NO:3	SGGAFDMRTL	MTNTLMKDQP	TLAVTFVDNH	DTEPGQALQS	WVDPWFKPLA	350
Figure 1	SGGAFDMRTL	MTNTLMKDQP	TLAVTFVDNH	DTEPGQALQS	WVDPWFKPLA	350
ATCC 31,195	SGGAFDMRTL	MTNTLMKDQP	TLAVTFVDNH	DTEPGQALQS	WVDPWFKPLA	350

Spezyme	YAFILTRQEG	YPCVFYGDYY	GIPQYNIPSL	KSKIDPLLIA	RRDYAYGTQH	398
SEQ ID NO:3	YAFILTRQEG	YPCVFYGDYY	GIPQYNIPSL	KSKIDPLLIA	RRDYAYGTQH	400
Figure 1	YAFILTRQEG	YPCVFYGDYY	GIPQYNIPSL	KSKIDPLLIA	RRDYAYGTQH	400
ATCC 31,195	YAFILTRQEG	YPCVFYGDYY	GIPQYNIPSL	KSKIDPLLIA	RRDYAYGTQH	400

Spezyme	DYLDHSDIIG	WTREGVTEKP	GSGLAALITD	GPGGSKWMYV	GKQHAGKVFY	448
SEQ ID NO:3	DYLDHSDIIG	WTREGVTEKP	GSGLAALITD	GPGGSKWMYV	GKQHAGKVFY	450
Figure 1	DYLDHSDIIG	WTREGVTEKP	GSGLAALITD	GPGGSKWMYV	GKQHAGKVFY	450
ATCC 31,195	DYLDHSDIIG	WTREGVTEKP	GSGLAALITD	GPGGSKWMYV	GKQHAGKVFY	450

Spezyme	DLTGNRSDTV	TINSDGWGEF	KVNGGSVSVW	VPRKTT		484
SEQ ID NO:3	DLTGNRSDTV	TINSDGWGEF	KVNGGSVSVW	VPRKTTVSTI	AWSITTRPWT	500
Figure 1	DLTGNRSDTV	TINSDGWGEF	KVNGGSVSVW	VPRKTTVSTI	ARPITTRPWT	500
ATCC 31,195	DLTGNRSDTV	TINSDGWGEF	KVNGGSVSVW	VPRKTTVST		486

Spezyme						
SEQ ID NO:3	DEFVRWTEPR	LVAW				514
Figure 1	GEFVRWTEPR	LVAW				514
ATCC 31,195						

EXHIBIT D